

## SEQUENCE LISTING

<110> Presnell, Scott R.  
 Xu, Wenfeng  
 Kindsvogel, Wayne  
 Chen, Zhi

<120> Mouse Cytokine Receptor

<130> 01-08

<150> US 60/273,035

<151> 2001-03-02

<150> US 60/279,232

<151> 2001-03-27

<160> 49

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2149

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(693)

<400> 1

atg atg cct aaa cat tgc ttt cta ggc ttc ctc atc agt ttc ttc ctt	48
Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu	
1                    5                    10                    15	

act ggt gta gca gga act cag tca acg cat gag tct ctg aag cct cag	96
Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln	
20                    25                    30	

agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag	144
---	-----

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln	
35 40 45	
cct ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac	192
Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr	
50 55 60	
aaa ata tat gga cag aga caa tgg aaa aat aaa gaa gac tgt tgg ggt	240
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly	
65 70 75 80	
act caa gaa ctc tct tgt gac ctt acc agt gaa acc tca gac ata cag	288
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln	
85 90 95	
gaa cct tat tac ggg agg gtg agg gcg gcc tcg gct ggg agc tac tca	336
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser	
100 105 110	
gaa tgg agc atg acg ccg cgg ttc act ccc tgg tgg gaa aca aaa ata	384
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile	
115 120 125	
gat cct cca gtc atg aat ata acc caa gtc aat ggc tct ttg ttg gta	432
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val	
130 135 140	
att ctc cat gct cca aat tta cca tat aga tac caa aag gaa aaa aat	480
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn	
145 150 155 160	
gta tct ata gaa gat tac tat gaa cta cta tac cga gtt ttt ata att	528
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile	
165 170 175	
aac aat tca cta gaa aag gag caa aag gtt tat gaa ggg gct cac aga	576
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg	
180 185 190	
gcg gtt gaa att gaa gct cta aca cca cac tcc agc tac tgt gta gtg	624
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val	
195 200 205	

gct gaa ata tat cag ccc atg tta gac aga aga agt cag aga agt gaa 672  
 Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu  
 210 215 220

gag aga tgt gtg gaa att cca tgacttggtg aatttgcat tcagcaatgt 723  
 Glu Arg Cys Val Glu Ile Pro  
 225 230

ggaaattcta aagctccctg agaacaggat gactcgtgtt tgaaggatct tatttaaaat 783  
 tgtttttgta ttttcttaaa gcaatattca ctgttacacc ttggggactt ctttgtttat 843  
 ccattctttt atcctttata tttcatttta aactatattt gaacgacatt ccccccgaag 903  
 aattgaaatg taaagatgag gcagagaata aagtgttcta tgaaattcag aactttattt 963  
 ctgaatgtaa catccctaata aacaaccttc attcttctaa tacagcaaaa taaaaattta 1023  
 acaaccaagg aatagtattt aagaaaatgt tgaaataatt tttttaaaat agcattacag 1083  
 actgaggcgg tcctgaagca atgggttttc actctcttat tgagccaatt aaattgacat 1143  
 tgctttgaca atttaaaact tctataaagg tgaatatttt tcatacattt ctattttata 1203  
 tgaatatact ttttatatat ttattattat taaatatttc tacttaatga atcaaaattt 1263  
 tgttttaaag tctactttat gtaaataaga acagggtttg gggaaaaaaa tcttatgatt 1323  
 tctggattga tatctgaatt aaaactatca acaacaagga agtctactct gtacaattgt 1383  
 ccctcattta aaagatatat taagcttttc ttttctgttt gtttttgttt tgtttagttt 1443  
 ttaatcctgt cttagaagaa cttatcttta ttctcaaaat taaatgtaat ttttttagtg 1503  
 acaaagaaga aaggaaacct cattactcaa tccttctggc caagagtgtc ttgcttgagg 1563  
 cgccttcctc atctctatat aggaggatcc catgaatgat ggtttattgg gaactgctgg 1623  
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 gccctcctg ctactgcct ctctgagta gaaatctggg gacctaaggc tcagtgcggt 1803  
 caacagaaag ctgccttctt cacttgaggc taagtcttca tatatgttta aggttgtctt 1863  
 tctagtgagg agatacatat cagagaacat ttgtacaatt ccccatgaaa attgctccaa 1923  
 agttgataac aatatagtcg gtgcttctag ttatatgcaa gtactcagtg ataaatggat 1983  
 taaaaaatat tcagaaatgt attggggggg ggaggagaat aagaggcaga gcaagagcta 2043  
 gagaattggt ttccttgctt ccctgtatgc tcagaaaaca ttgatttgag catagacgca 2103  
 gagactgaaa aaaaaaaaaat gctcgagcgg ccgccatatc cttggt 2149

<210> 2

<211> 231

<212> PRT

<213> Homo sapiens

<400> 2

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu  
 1 5 10 15  
 Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln  
 20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln  
 35 40 45  
 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr  
 50 55 60  
 Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly  
 65 70 75 80  
 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln  
 85 90 95  
 Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser  
 100 105 110  
 Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile  
 115 120 125  
 Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val  
 130 135 140  
 Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn  
 145 150 155 160  
 Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile  
 165 170 175  
 Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg  
 180 185 190  
 Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val  
 195 200 205  
 Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu  
 210 215 220  
 Glu Arg Cys Val Glu Ile Pro  
 225 230

<210> 3

<211> 693

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the  
amino acid sequence of SEQ ID NO:2

<221> misc\_feature

<222> (1)...(693)

<223> n = A,T,C or G

<400> 3

atgatgccna arcaytgytt yytnggntty ytnathwsnt tyttyytnac nggngtngcn 60  
 ggnacncarw snacncayga rwsnytnaar ccncarmng tncarttyca rwsnmgnaay 120

ttycayaaya	thytncartg	gcarccnggn	mgngcnytna	cnggnaayws	nwsngtntay	180
ttygtncart	ayaarathta	yggncarmgn	cartggaara	ayaargarga	ytgytggggg	240
acncargary	tnwsntgyga	yytnacnwsn	garacnwsng	ayathcarga	rccntaytay	300
ggnmgngtnm	gngcngcnws	ngcnggnwsn	taywsngart	ggwsnatgac	nccnmgnnty	360
acnccntggg	gggaracnaa	rathgayccn	ccngtnatga	ayathacna	rgtnaayggg	420
wsnytnytn	tnathytnca	ygcncnaay	ytncntaym	gntaycaraa	rgaraaraay	480
gtnwsnathg	argaytayta	ygarytnytn	taymngntnt	tyathathaa	yaaywsnytn	540
garaargarc	araargnta	ygargngcn	caymngngcng	tngarathga	rgcnytnacn	600
ccncaywsnw	sntaytgygt	ngtngcngar	athtaycarc	cnatgytnga	ymgnmgnwsn	660
carmgnwsng	argarmgntg	ygtngarath	ccn			693

&lt;210&gt; 4

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Peptide linker.

&lt;400&gt; 4

Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
1			5					10						15	

&lt;210&gt; 5

&lt;211&gt; 699

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

gagcccagat	cttcagacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaagccgag	60
ggggcaccgt	cagtcttcct	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	120
acccttgagg	tcacatgctg	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagtgc	180
aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccgcg	ggaggagcag	240
tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaccagga	ctggctgaat	300
ggcaaggagt	acaagtgcaa	ggtctccaac	aaagccctcc	catcttccat	cgagaaaacc	360
atctccaaag	ccaaagggca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccgg	420
gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatcccagc	480
gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	540
cccgtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcaccgt	ggacaagagc	600
aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	660
tacacgcaga	agagcctctc	cctgtctccg	ggtaaataa			699

&lt;210&gt; 6

<211> 32  
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 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC29181

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<210> 7  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC29182

<400> 7  
 gcagatcttg gaatttcac acatctctct tca 33

<210> 8  
 <211> 108  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(108)

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 atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt ggc 48  
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly  
 1 5 10 15

gcc gtc ttc gtt tcg ctc agc cag gaa atc cat gcc gag ttg aga cgc 96  
 Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg  
 20 25 30

ttc cgt aga tcc 108  
 Phe Arg Arg Ser  
 35

<210> 9  
 <211> 36  
 <212> PRT  
 <213> Homo sapiens

<400> 9  
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly  
 1 5 10 15  
 Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg  
 20 25 30  
 Phe Arg Arg Ser  
 35

<210> 10  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Glu-Glu (CEE) Tag amino acid sequence

<400> 10  
 Glu Tyr Met Pro Met Glu  
 1 5

<210> 11  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> FLAG Tag amino acid sequence

<400> 11  
 Asp Tyr Lys Asp Asp Asp Asp Lys  
 1 5

<210> 12  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; His Tag amino acid sequence

&lt;400&gt; 12

His His His His His His

1

5

&lt;210&gt; 13

&lt;211&gt; 210

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 13

Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln Arg Val Gln Phe Gln  
 1 5 10 15  
 Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln Pro Gly Arg Ala Leu  
 20 25 30  
 Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr Lys Ile Tyr Gly Gln  
 35 40 45  
 Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly Thr Gln Glu Leu Ser  
 50 55 60  
 Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln Glu Pro Tyr Tyr Gly  
 65 70 75 80  
 Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser Glu Trp Ser Met Thr  
 85 90 95  
 Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile Asp Pro Pro Val Met  
 100 105 110  
 Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val Ile Leu His Ala Pro  
 115 120 125  
 Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn Val Ser Ile Glu Asp  
 130 135 140  
 Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile Asn Asn Ser Leu Glu  
 145 150 155 160  
 Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg Ala Val Glu Ile Glu  
 165 170 175  
 Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val Ala Glu Ile Tyr Gln  
 180 185 190  
 Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu Glu Arg Cys Val Glu  
 195 200 205  
 Ile Pro  
 210

&lt;210&gt; 14



<220>  
<221> CDS  
<222> (21)...(557)

tcgagttaga attgtctgca atg gcc gcc ctg cag aaa tct gtg agc tct ttc 53  
Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe  
1 5 10

gta cag gga gga gca gct gcg ccc atc agc tcc cac tgc agg ctt gac 149  
Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp  
30 35 40

gct aag gag gct agc ttg gct gat aac aac aca gac gtt cgt ctc att 245  
Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile  
60 65 70 75

atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa 341  
Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln  
95 100 105

agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg 437  
Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu

125

130

135

cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt 485  
 His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu  
 140 145 150 155

gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt 533  
 Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe  
 160 165 170

atg tct ctg aga aat gcc tgc att tgaccagagc aaagctgaaa aatgaataac 587  
 Met Ser Leu Arg Asn Ala Cys Ile  
 175

taacccccctt tccctgctag aaataacaat tagatgcccc aaagcgattt tttttaacca 647  
 aaaggaagat gggaagccaa actccatcat gatgggtgga ttccaaatga acccctgcgt 707  
 tagttacaaa ggaaaccaat gccacttttg tttataagac cagaaggtag acttttctaag 767  
 catagatatt tattgataac atttcattgt aactgggtgt ctatacacag aaaacaattt 827  
 attttttaaa taattgtctt tttccataaa aaagattact ttccattcct ttaggggaaa 887  
 aaacccttaa atagcttcat gtttccataa tcagtacttt atattttataa atgtatttat 947  
 tattattata agactgcatt ttattttatat cattttatta atatggattt atttatagaa 1007  
 acatcattcg atattgctac ttgagtgtaa ggctaataat gatatttatg acaataatta 1067  
 tagagctata acatgtttat ttgacctcaa taaacacttg gatatccta 1116

&lt;210&gt; 15

&lt;211&gt; 179

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 15

Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe Leu Met Gly Thr Leu  
 1 5 10 15  
 Ala Thr Ser Cys Leu Leu Leu Ala Leu Leu Val Gln Gly Gly Ala  
 20 25 30  
 Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln  
 35 40 45  
 Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser  
 50 55 60  
 Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe  
 65 70 75 80  
 His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu  
 85 90 95  
 Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln

100 105 110  
 Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg  
 115 120 125  
 Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn  
 130 135 140  
 Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu  
 145 150 155 160  
 Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn  
 165 170 175  
 Ala Cys Ile

<210> 16  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC25963

<400> 16  
 agtcaacgca tgagtctctg aag

23

<210> 17  
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 <212> DNA  
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<220>  
 <223> Oligonucleotide primer ZC28354

<400> 17  
 accaacaag agccattgac ttg

23

<210> 18  
 <211> 23  
 <212> DNA  
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<220>  
 <223> Oligonucleotide primer ZC21195

<400> 18

gaggagacca taacccccga cag

23

<210> 19

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC21196

<400> 19

catagctccc accacacgat ttt

23

<210> 20

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC14063

<400> 20

caccagacat aatagctgac agact

25

<210> 21

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC17574

<400> 21

ggtrttgctc agcatgcaca c

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<210> 22

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC17600

<400> 22

catgtaggcc atgaggtcca ccac

24

<210> 23

<211> 22

<212> DNA

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 $\langle 220 \rangle$ 

<223> Oligonucleotide primer ZC27659

<400> 23

tcaagctgag ttctctgtat gg

22

<210> 24

<211> 2831

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (34)...(1755)

<400> 24

tagaggccaa gggagggctc tgtgccagcc ccg atg agg acg ctg ctg acc atc 54

Met Arg Thr Leu Leu Thr Ile

1

5

ttg act gtg gga tcc ctg gct gct cac gcc cct gag gac ccc tcg gat 102

Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp

10

15

20

ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg 150

Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu

25

30

35

acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc 198

Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile

40

45

50

55

gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt 246

Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys

60

65

70

cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag acg ggc aac Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn 75 80 85	294
ctc acg gag ctc tac tat gcc agg gtc acc gct gtc agt gcg gga ggc Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly 90 95 100	342
cgg tca gcc acc aag atg act gac agg ttc agc tct ctg cag cac act Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr 105 110 115	390
acc ctc aag cca cct gat gtg acc tgt atc tcc aaa gtg aga tcg att Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile 120 125 130 135	438
cag atg att gtt cat cct acc ccc acg cca atc cgt gca ggc gat ggc Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly 140 145 150	486
cac cgg cta acc ctg gaa gac atc ttc cat gac ctg ttc tac cac tta His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu 155 160 165	534
gag ctc cag gtc aac cgc acc tac caa atg cac ctt gga ggg aag cag Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln 170 175 180	582
aga gaa tat gag ttc ttc ggc ctg acc cct gac aca gag ttc ctt ggc Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly 185 190 195	630
acc atc atg att tgc gtt ccc acc tgg gcc aag gag agt gcc ccc tac Thr Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr 200 205 210 215	678
atg tgc cga gtg aag aca ctg cca gac cgg aca tgg acc tac tcc ttc Met Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe 220 225 230	726
tcc gga gcc ttc ctg ttc tcc atg ggc ttc ctc gtc gca gta ctc tgc Ser Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys	774

235	240	245	
tac ctg agc tac aga tat gtc acc aag ccg cct gca cct ccc aac tcc Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Pro Asn Ser 250 255 260			822
ctg aac gtc cag cga gtc ctg act ttc cag ccg ctg cgc ttc atc cag Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln 265 270 275			870
gag cac gtc ctg atc cct gtc ttt gac ctc agc ggc ccc agc agt ctg Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu 280 285 290 295			918
gcc cag cct gtc cag tac tcc cag atc agg gtg tct gga ccc agg gag Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu 300 305 310			966
ccc gca gga gct cca cag cgg cat agc ctg tcc gag atc acc tac tta Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu 315 320 325			1014
ggg cag cca gac atc tcc atc ctc cag ccc tcc aac gtg cca cct ccc Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro 330 335 340			1062
cag atc ctc tcc cca ctg tcc tat gcc cca aac gct gcc cct gag gtc Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val 345 350 355			1110
ggg ccc cca tcc tat gca cct cag gtg acc ccc gaa gct caa ttc cca Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro 360 365 370 375			1158
ttc tac gcc cca cag gcc atc tct aag gtc cag cct tcc tcc tat gcc Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala 380 385 390			1206
cct caa gcc act ccg gac agc tgg cct ccc tcc tat ggg gta tgc atg Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met 395 400 405			1254
gaa ggt tct ggc aaa gac tcc ccc act ggg aca ctt tct agt cct aaa			1302

Glu Gly Ser Gly Lys Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Lys	
410	415 420
cac ctt agg cct aaa ggt cag ctt cag aaa gag cca cca gct gga agc	1350
His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser	
425	430 435
tgc atg tta ggt ggc ctt tct ctg cag gag gtg acc tcc ttg gct atg	1398
Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met	
440	445 450 455
gag gaa tcc caa gaa gca aaa tca ttg cac cag ccc ctg ggg att tgc	1446
Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys	
460	465 470
aca gac aga aca tct gac cca aat gtg cta cac agt ggg gag gaa ggg	1494
Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly	
475	480 485
aca cca cag tac cta aag ggc cag ctc ccc ctc ctc tcc tca gtc cag	1542
Thr Pro Gln Tyr Leu Lys Gly Gln Leu Pro Leu Leu Ser Ser Val Gln	
490	495 500
atc gag ggc cac ccc atg tcc ctc cct ttg caa cct cct tcc ggt cca	1590
Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro	
505	510 515
tgt tcc ccc tcg gac caa ggt cca agt ccc tgg ggc ctg ctg gag tcc	1638
Cys Ser Pro Ser Asp Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser	
520	525 530 535
ctt gtg tgt ccc aag gat gaa gcc aag agc cca gcc cct gag acc tca	1686
Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser	
540	545 550
gac ctg gag cag ccc aca gaa ctg gat tct ctt ttc aga ggc ctg gcc	1734
Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala	
555	560 565
ctg act gtg cag tgg gag tcc tgaggggaat gggaaaggct tggtgcttcc	1785
Leu Thr Val Gln Trp Glu Ser	
570	



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tccctgtccc taccagtggt cacatccttg gctgtcaatc ccatgcctgc ccatgccaca 1845
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gggagctctg gggagcagct tgtgtagaca agcgcgtgct cgctgagccc tgcaaggcag 2025
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&lt;210&gt; 25

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 25

```

Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
1           5           10          15
Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
20          25          30
Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
35          40          45
Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
50          55          60
Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
65          70          75          80
Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
85          90          95
Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
100         105         110
Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
115         120         125
Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
130         135         140

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Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe  
 145 150 155 160  
 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln  
 165 170 175  
 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr  
 180 185 190  
 Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp  
 195 200 205  
 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp  
 210 215 220  
 Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly  
 225 230 235 240  
 Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys  
 245 250 255  
 Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe  
 260 265 270  
 Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp  
 275 280 285  
 Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro Val Gln Tyr Ser Gln Ile  
 290 295 300  
 Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Pro Gln Arg His Ser  
 305 310 315 320  
 Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro Asp Ile Ser Ile Leu Gln  
 325 330 335  
 Pro Ser Asn Val Pro Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala  
 340 345 350  
 Pro Asn Ala Ala Pro Glu Val Gly Pro Pro Ser Tyr Ala Pro Gln Val  
 355 360 365  
 Thr Pro Glu Ala Gln Phe Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys  
 370 375 380  
 Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro  
 385 390 395 400  
 Pro Ser Tyr Gly Val Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr  
 405 410 415  
 Gly Thr Leu Ser Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln  
 420 425 430  
 Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln  
 435 440 445  
 Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu  
 450 455 460  
 His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val  
 465 470 475 480  
 Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu

485 490 495  
 Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro  
 500 505 510  
 Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser  
 515 520 525  
 Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys  
 530 535 540  
 Ser Pro Ala Pro Glu Thr Ser Asp Leu Glu Gln Pro Thr Glu Leu Asp  
 545 550 555 560  
 Ser Leu Phe Arg Gly Leu Ala Leu Thr Val Gln Trp Glu Ser  
 565 570

&lt;210&gt; 26

&lt;211&gt; 39

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide linker ZC13252

&lt;400&gt; 26

ggcctgaaag cttcggataa tgaaggtacc tgtagaaa

39

&lt;210&gt; 27

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide linker ZC13453

&lt;400&gt; 27

ttaggatccg gcccttcccc agatact

27

&lt;210&gt; 28

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC28590

&lt;400&gt; 28

ttgggtacct ctgcaatggc cgccctgcag aaatct 36

<210> 29

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC28580

<400> 29

ttgggatcca atgcagggcat ttctcagaga cat 33

<210> 30

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC25963

<400> 30

agtcaacgca tgagtctctg aag 23

<210> 31

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC25964

<400> 31

gttcttgagt accccaacag tct 23

<210> 32

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC14666

&lt;400&gt; 32

agccaccaag atgactga

18

&lt;210&gt; 33

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC14742

&lt;400&gt; 33

tgcatttggt aggtgcggtt ga

22

&lt;210&gt; 34

&lt;211&gt; 211

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 34

Pro	Glu	Asp	Pro	Ser	Asp	Leu	Leu	Gln	His	Val	Lys	Phe	Gln	Ser	Ser	1	5	10	15
Asn	Phe	Glu	Asn	Ile	Leu	Thr	Trp	Asp	Ser	Gly	Pro	Glu	Gly	Thr	Pro	20	25	30	
Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp	Trp	35	40	45	
Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn	Leu	50	55	60	
Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val	Thr	65	70	75	80
Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg	Phe	85	90	95	
Ser	Ser	Leu	Gln	His	Thr	Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys	Ile	100	105	110	
Ser	Lys	Val	Arg	Ser	Ile	Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr	Pro	115	120	125	
Ile	Arg	Ala	Gly	Asp	Gly	His	Arg	Leu	Thr	Leu	Glu	Asp	Ile	Phe	His	130	135	140	
Asp	Leu	Phe	Tyr	His	Leu	Glu	Leu	Gln	Val	Asn	Arg	Thr	Tyr	Gln	Met	145	150	155	160
His	Leu	Gly	Gly	Lys	Gln	Arg	Glu	Tyr	Glu	Phe	Phe	Gly	Leu	Thr	Pro	165	170	175	
Asp	Thr	Glu	Phe	Leu	Gly	Thr	Ile	Met	Ile	Cys	Val	Pro	Thr	Trp	Ala				

180 185 190  
 Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp Arg  
 195 200 205  
 Thr Trp Thr  
 210

<210> 35  
 <211> 199  
 <212> PRT  
 <213> Homo sapiens

<400> 35  
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 20 25 30  
 Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp Lys Cys Met  
 35 40 45  
 Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly  
 50 55 60  
 Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp  
 65 70 75 80  
 Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro  
 85 90 95  
 Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe  
 100 105 110  
 Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn  
 115 120 125  
 Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr  
 130 135 140  
 Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg  
 145 150 155 160  
 Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu  
 165 170 175  
 Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln  
 180 185 190  
 Thr Thr His Asp Glu Thr Val  
 195

<210> 36  
 <211> 211  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 36

Ser Asp Ala His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe  
 1 5 10 15  
 Glu Ala Glu Phe Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn  
 20 25 30  
 Gln Ser Glu Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile  
 35 40 45  
 Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp  
 50 55 60  
 Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala  
 65 70 75 80  
 Arg Val Arg Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr  
 85 90 95  
 Asn Thr Arg Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val  
 100 105 110  
 Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro  
 115 120 125  
 Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser  
 130 135 140  
 His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe  
 145 150 155 160  
 Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr  
 165 170 175  
 Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala  
 180 185 190  
 Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu  
 195 200 205  
 Thr Arg Gln  
 210

&lt;210&gt; 37

&lt;211&gt; 2464

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (8)...(697)

&lt;400&gt; 37

ggcaacc atg atg cct aag cat tgc ctt cta ggt ctc ctc atc ata ctc  
 Met Met Pro Lys His Cys Leu Leu Gly Leu Leu Ile Ile Leu

1	5	10	
ttg agc agt gca aca gaa ata caa cca gct cgt gta tct ctg acg ctc			97
Leu Ser Ser Ala Thr Glu Ile Gln Pro Ala Arg Val Ser Leu Thr Leu			
15	20	25	30
cag aag gtc cga ttt cag tcc aga aat ttc cac aat att ttg cac tgg			145
Gln Lys Val Arg Phe Gln Ser Arg Asn Phe His Asn Ile Leu His Trp			
	35	40	45
caa gca ggg agc tct ctc ccc agc aac aac agc atc tac ttt gtg cag			193
Gln Ala Gly Ser Ser Leu Pro Ser Asn Asn Ser Ile Tyr Phe Val Gln			
	50	55	60
tac aag atg tat gga cag agc caa tgg gaa gat aaa gtt gac tgc tgg			241
Tyr Lys Met Tyr Gly Gln Ser Gln Trp Glu Asp Lys Val Asp Cys Trp			
	65	70	75
ggg acc acg gcg ctc ttc tgt gac ctg acc aat gaa acc tta gac cca			289
Gly Thr Thr Ala Leu Phe Cys Asp Leu Thr Asn Glu Thr Leu Asp Pro			
	80	85	90
tac gag ctg tat tac ggg agg gtg atg acg gcc tgt gct gga cgc cac			337
Tyr Glu Leu Tyr Tyr Gly Arg Val Met Thr Ala Cys Ala Gly Arg His			
	95	100	105
tct gcc tgg acc agg aca ccc cgc ttc act cca tgg tgg gaa aca aaa			385
Ser Ala Trp Thr Arg Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys			
	115	120	125
cta gat cct ccg gtc gtg act ata acc cga gtt aac gca tct ttg cgg			433
Leu Asp Pro Pro Val Val Thr Ile Thr Arg Val Asn Ala Ser Leu Arg			
	130	135	140
gtg ctt ctc cgt cct cca gag ttg cca aat aga aac caa agt gga aaa			481
Val Leu Leu Arg Pro Pro Glu Leu Pro Asn Arg Asn Gln Ser Gly Lys			
	145	150	155
aat gca tcc atg gaa act tac tac ggc tta gta tac aga gtt ttc aca			529
Asn Ala Ser Met Glu Thr Tyr Tyr Gly Leu Val Tyr Arg Val Phe Thr			
	160	165	170
atc aac aat tca cta gag aag gag caa aaa gcc tat gaa gga act cag			577



Ile Asn Asn Ser Leu Glu Lys Glu Gln Lys Ala Tyr Glu Gly Thr Gln  
175 180 185 190

aga gct gtt gaa att gaa ggt ctg ata cct cat tcc agc tac tgc gta 625  
Arg Ala Val Glu Ile Glu Gly Leu Ile Pro His Ser Ser Tyr Cys Val  
195 200 205

gtg gct gaa atg tac cag ccc atg ttt gac aga aga agc cca aga agc 673  
Val Ala Glu Met Tyr Gln Pro Met Phe Asp Arg Arg Ser Pro Arg Ser  
210 215 220

aag gag aga tgt gtg cag att cca tgaactggctc tgaggcgcta aaaccggaag 727  
Lys Glu Arg Cys Val Gln Ile Pro  
225 230

catattgaga acaggatgtc ttctgcctag aacagcttac taaacttctg ttttgatttt 787  
cttagagcaa tgtctaccca cacttttcaa ggatttcttt gtcagtactt tcttttctgt 847  
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aactctgaaa agtatagtgc gtacgtctgt cttcttacgt tttttaatgg taaatggtca 1987  
cagaccatta agaacataag agacatgtga aaagcaagag cattgtcctg gctgtcctgt 2047  
gtgttcagaa aacactggcc ttcatcttta tttttgaatt attcaatttt tatttctttt 2107  
gtggcttagt acctgcttgg gaattctttg ggttttttgt tcgttgtttg tttattttct 2167  
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aggcaattgt tggtttatga gtgttgctag caatcagagt tttgctttga ctttgtttgc 2347  
ttgggttttc cctcacacaa gtataagatg ctttgaaata tattacgatt ttcacattct 2407

ggatcatgtt aagaatatat tgtctaagta cttcaataaa tcttactttg tacttta

2464

<210> 38

<211> 230

<212> PRT

<213> Mus musculus

<400> 38

Met Met Pro Lys His Cys Leu Leu Gly Leu Leu Ile Ile Leu Leu Ser  
 1 5 10 15  
 Ser Ala Thr Glu Ile Gln Pro Ala Arg Val Ser Leu Thr Leu Gln Lys  
 20 25 30  
 Val Arg Phe Gln Ser Arg Asn Phe His Asn Ile Leu His Trp Gln Ala  
 35 40 45  
 Gly Ser Ser Leu Pro Ser Asn Asn Ser Ile Tyr Phe Val Gln Tyr Lys  
 50 55 60  
 Met Tyr Gly Gln Ser Gln Trp Glu Asp Lys Val Asp Cys Trp Gly Thr  
 65 70 75 80  
 Thr Ala Leu Phe Cys Asp Leu Thr Asn Glu Thr Leu Asp Pro Tyr Glu  
 85 90 95  
 Leu Tyr Tyr Gly Arg Val Met Thr Ala Cys Ala Gly Arg His Ser Ala  
 100 105 110  
 Trp Thr Arg Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Leu Asp  
 115 120 125  
 Pro Pro Val Val Thr Ile Thr Arg Val Asn Ala Ser Leu Arg Val Leu  
 130 135 140  
 Leu Arg Pro Pro Glu Leu Pro Asn Arg Asn Gln Ser Gly Lys Asn Ala  
 145 150 155 160  
 Ser Met Glu Thr Tyr Tyr Gly Leu Val Tyr Arg Val Phe Thr Ile Asn  
 165 170 175  
 Asn Ser Leu Glu Lys Glu Gln Lys Ala Tyr Glu Gly Thr Gln Arg Ala  
 180 185 190  
 Val Glu Ile Glu Gly Leu Ile Pro His Ser Ser Tyr Cys Val Val Ala  
 195 200 205  
 Glu Met Tyr Gln Pro Met Phe Asp Arg Arg Ser Pro Arg Ser Lys Glu  
 210 215 220  
 Arg Cys Val Gln Ile Pro  
 225 230

<210> 39

<211> 690

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Degenerate polynucleotide sequence of SEQ ID NO:38

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(690)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 39

atgatgccna arcaytgyyt nytnngnytn ytnathathy tnytnwsnws ngcnacngar	60
athcarccng cnmgngtnws nytnacnytn caraargtnm gnttycarws nmгнаaytty	120
cayaayathy tncaytggca rgcnngnwsn wsnytnccnw snaayaayws nathtaytty	180
gtncartaya aratgtaygg ncarwsncar tgggargaya argtngaytg ytggggnacn	240
acngcnytn tytgygayt nacnaaygar acnytngayc cntaygaryt ntaytaygg	300
mgngtnatga cngcntgygc nggnmgncay wsngcntgga cnmgnacncc nmgnattyacn	360
ccntgggtggg aracnaaryt ngayccnccn gtngtnacna thacnmngnt naaygcwnsn	420
ytnmgngtny tnytnmgnc nccngarytn ccnaaymgna aycarwsngg naaraaygc	480
wsnatggara cntaytaygg nytngtntay mgngtnttya cnathaayaa ywsnytngar	540
aargarcara argcntayga rggnacncar mgngcngtn arathgargg nytnathccn	600
caywsnwsnt aytgygtngt ngcngaratg taycarccna tgattygaymg nmgnwsnccn	660
mgwnsnaarg armgntgygt ncarathccn	690

&lt;210&gt; 40

&lt;211&gt; 1050

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (50)...(589)

&lt;400&gt; 40

aacaggctct cctctcactt atcaactttt gacacttggt cgatcgggtg atg gct gtc	58
	Met Ala Val
	1
ctg cag aaa tct atg agt ttt tcc ctt atg ggg act ttg gcc gcc agc	106
Leu Gln Lys Ser Met Ser Phe Ser Leu Met Gly Thr Leu Ala Ala Ser	
5 10 15	
tgc ctg ctt ctc att gcc ctg tgg gcc cag gag gca aat gcg ctg ccc	154
Cys Leu Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn Ala Leu Pro	
20 25 30 35	

atc aac acc cgg tgc aag ctt gag gtg tcc aac ttc cag cag ccg tac 202  
 Ile Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln Gln Pro Tyr  
 40 45 50

atc gtc aac cgc acc ttt atg ctg gcc aag gag gcc agc ctt gca gat 250  
 Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu Ala Asp  
 55 60 65

aac aac aca gac gtc cgg ctc atc ggg gag aaa ctg ttc cga gga gtc 298  
 Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe Arg Gly Val  
 70 75 80

agt gct aag gat cag tgc tac ctg atg aag cag gtg ctc aac ttc acc 346  
 Ser Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu Asn Phe Thr  
 85 90 95

ctg gaa gac att ctg ctc ccc cag tca gac agg ttc cgg ccc tac atg 394  
 Leu Glu Asp Ile Leu Leu Pro Gln Ser Asp Arg Phe Arg Pro Tyr Met  
 100 105 110 115

cag gag gtg gtg cct ttc ctg acc aaa ctc agc aat cag ctc agc tcc 442  
 Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln Leu Ser Ser  
 120 125 130

tgt cac atc agt ggt gac gac cag aac atc cag aag aat gtc aga agg 490  
 Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn Val Arg Arg  
 135 140 145

ctg aag gag aca gtg aaa aag ctt gga gag agc gga gag atc aaa gcg 538  
 Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu Ile Lys Ala  
 150 155 160

atc ggg gaa ctg gac ctg ctg ttt atg tct ctg aga aat gct tgc gtc 586  
 Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn Ala Cys Val  
 165 170 175

tga gcgagaagaa gctagaaaac gaagaactgc tccttcctgc cttctaaaaa 639  
 \*

gaacaataag atccctgaat ggactttttt actaaaggaa agtgagaagc taacgtccac 699  
 catcattaga agatttcaca tgaaacctgg ctcagttgaa agagaaaata gtgtcaagtt 759

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gtccatgaga ccagaggtag acttgataac cacaaagatt cattgacaat attttattgt      819
cattgataat gcaacagaaa aagtatgtac tttaaaaaat tgtttgaaag gaggttacct      879
ctcattcctc tagaagaaaa gcctatgtaa cttcatttcc ataaccaata ctttatatat      939
gtaagtttat ttattataag tatacatttt atttatgtca gtttattaat atggatttat      999
ttatagaaaa attatctgat gttgatattt gagtataaag caaataatat t                1050

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<210> 41  
 <211> 179  
 <212> PRT  
 <213> Mus musculus

<400> 41

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Met Ala Val Leu Gln Lys Ser Met Ser Phe Ser Leu Met Gly Thr Leu
 1              5              10              15
Ala Ala Ser Cys Leu Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn
      20              25              30
Ala Leu Pro Ile Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln
      35              40              45
Gln Pro Tyr Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
      50              55              60
Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
65              70              75              80
Arg Gly Val Ser Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu
      85              90              95
Asn Phe Thr Leu Glu Asp Ile Leu Leu Pro Gln Ser Asp Arg Phe Arg
      100             105             110
Pro Tyr Met Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln
      115             120             125
Leu Ser Ser Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn
      130             135             140
Val Arg Arg Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
      145             150             155             160
Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
      165             170             175
Ala Cys Val

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<210> 42  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC10651

<400> 42

agcttttctg cagcagctct

20

<210> 43

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC10565

<400> 43

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23

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC38001

<400> 44

ccgttcgtga ctataacccg

20

<210> 45

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC38022

<400> 45

agccgtagta agtttccat

19

<210> 46

<211> 4

<212> PRT

<213> Artificial Sequence

<223> SXWS polypeptide motif

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<223> Xaa = Any Amino Acid

Ser Xaa Trp Ser

1

<211> 707

<213> Mus musculus

<221> CDS

<222> (2) ... (691)

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Met Met Pro Lys His Cys Leu Leu Gly Leu Leu Ile Ile Leu Leu Ser  
1 5 10 15

agt gca aca gaa ata caa cca gct cgt gta tct ctg acg ccc cag aag 97  
 Ser Ala Thr Glu Ile Gln Pro Ala Arg Val Ser Leu Thr Pro Gln Lys  
 20 25 30

gtc cga ttt cag tcc aga aat ttc cac aat att ttg cac tgg caa gca 145  
Val Arg Phe Gln Ser Arg Asn Phe His Asn Ile Leu His Trp Gln Ala  
35 40 45

ggg agc tct ctc ccc agc aac aac agc atc tac ttt gtg cag tac aag 193  
Gly Ser Ser Leu Pro Ser Asn Asn Ser Ile Tyr Phe Val Gln Tyr Lys  
50 55 60

atg tat gga cag agc caa tgg gaa gat aaa gtt gac tgc tgg ggg acc 241  
Met Tyr Gly Gln Ser Gln Trp Glu Asp Lys Val Asp Cys Trp Gly Thr  
65 70 75 80

acg gcg ctc ttc tgt gac ctg acc aat gaa acc tta gac cca tac gag 289  
Thr Ala Leu Phe Cys Asp Leu Thr Asn Glu Thr Leu Asp Pro Tyr Glu

	85	90	95	
ctg tat tac ggg agg gtg atg acg gcc tgt gct gga cgc cac tct gcc				337
Leu Tyr Tyr Gly Arg Val Met Thr Ala Cys Ala Gly Arg His Ser Ala				
	100	105	110	
tgg acc agg aca ccc cgc ttc act cca tgg tgg gaa aca aaa cta gat				385
Trp Thr Arg Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Leu Asp				
	115	120	125	
cct ccg gtc gtg act ata acc cga gtt aac gca tct ttg cgg gtg ctt				433
Pro Pro Val Val Thr Ile Thr Arg Val Asn Ala Ser Leu Arg Val Leu				
	130	135	140	
ctc cgt cct cca gag ttg cca aat aga aac caa agt gga aaa aat gca				481
Leu Arg Pro Pro Glu Leu Pro Asn Arg Asn Gln Ser Gly Lys Asn Ala				
	145	150	155	160
tcc atg gaa act tac tac ggc tta gta tac aga gtt ttc aca atc aac				529
Ser Met Glu Thr Tyr Tyr Gly Leu Val Tyr Arg Val Phe Thr Ile Asn				
	165	170	175	
aat tca cta gag aag gag caa aaa gcc tat gaa gga act cag aga gct				577
Asn Ser Leu Glu Lys Glu Gln Lys Ala Tyr Glu Gly Thr Gln Arg Ala				
	180	185	190	
gtt gaa att gaa ggt ctg ata cct cat tcc agc tac tgc gta gtg gct				625
Val Glu Ile Glu Gly Leu Ile Pro His Ser Ser Tyr Cys Val Val Ala				
	195	200	205	
gaa atg tac cag ccc atg ttt gac aga aga agc cca aga agc aag gag				673
Glu Met Tyr Gln Pro Met Phe Asp Arg Arg Ser Pro Arg Ser Lys Glu				
	210	215	220	
aga tgt gtg cac att cca tgaactgggc tgaggc				707
Arg Cys Val His Ile Pro				
	225	230		

&lt;210&gt; 48

&lt;211&gt; 230

&lt;212&gt; PRT

&lt;213&gt; Mus musculus



&lt;400&gt; 48

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Met Met Pro Lys His Cys Leu Leu Gly Leu Leu Ile Ile Leu Leu Ser
 1      5      10      15
Ser Ala Thr Glu Ile Gln Pro Ala Arg Val Ser Leu Thr Pro Gln Lys
      20      25      30
Val Arg Phe Gln Ser Arg Asn Phe His Asn Ile Leu His Trp Gln Ala
      35      40      45
Gly Ser Ser Leu Pro Ser Asn Asn Ser Ile Tyr Phe Val Gln Tyr Lys
      50      55      60
Met Tyr Gly Gln Ser Gln Trp Glu Asp Lys Val Asp Cys Trp Gly Thr
65      70      75      80
Thr Ala Leu Phe Cys Asp Leu Thr Asn Glu Thr Leu Asp Pro Tyr Glu
      85      90      95
Leu Tyr Tyr Gly Arg Val Met Thr Ala Cys Ala Gly Arg His Ser Ala
      100      105      110
Trp Thr Arg Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Leu Asp
      115      120      125
Pro Pro Val Val Thr Ile Thr Arg Val Asn Ala Ser Leu Arg Val Leu
      130      135      140
Leu Arg Pro Pro Glu Leu Pro Asn Arg Asn Gln Ser Gly Lys Asn Ala
145      150      155      160
Ser Met Glu Thr Tyr Tyr Gly Leu Val Tyr Arg Val Phe Thr Ile Asn
      165      170      175
Asn Ser Leu Glu Lys Glu Gln Lys Ala Tyr Glu Gly Thr Gln Arg Ala
      180      185      190
Val Glu Ile Glu Gly Leu Ile Pro His Ser Ser Tyr Cys Val Val Ala
      195      200      205
Glu Met Tyr Gln Pro Met Phe Asp Arg Arg Ser Pro Arg Ser Lys Glu
      210      215      220
Arg Cys Val His Ile Pro
225      230

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&lt;210&gt; 49

&lt;211&gt; 690

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Degenerate polynucleotide sequence of SEQ ID NO:48

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(690)

<400> 49

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athcarccng	cnmgngtnws	nytnacncn	caraargtnm	gnattyarws	nmgnaaytty	120
cayaayathy	tncaytggca	rgcnngnwsn	wsnytnccnw	snaayaayws	nathtaytty	180
gtncartaya	aratgtaygg	ncarwsncar	tgggargaya	argtngaytg	ytggggnacn	240
acngcnytn	tytgygayyt	nacnaaygar	acnytngayc	cntaygaryt	ntaytayggn	300
mgngtnatga	cngcntgygc	nggnmgncay	wsngcntgga	cnmgnacncc	nmgnattyacn	360
ccntggtggg	aracnaaryt	ngayccncn	gtngtnacna	thacnmngnt	naaygcnwsn	420
ytnmgngtny	tnytnmgnc	ncngarytn	ccnaaymgna	aycarwsngg	naaraaygcn	480
wsnatggara	cntaytaygg	nytngtntay	mgngtnatty	cnathaayaa	ywsnytngar	540
aargarcara	argcntayga	rggnacncar	mgngcngtn	arathgargg	nytnathccn	600
caywsnwsnt	aytgygtngt	ngcngaratg	taycarccna	tgtygaymg	nmgnwsnccn	660
mgnwsnaarg	armgntgygt	ncayathccn				690